

Legends to Supplementary Figures

Figure S1: Discriminant Analysis of Principal Components on microsatellite allele frequencies for A) The Americas, B) United States of America (excluding Exeter population), c) Mexico, and D) South America.

Figure S2: Evolutionary scenarios of *Aedes aegypti aegypti* re-colonization of Rabai, Kenya, evaluated using Approximate Bayesian Computation inference as implemented by the DIYABC software (Cornuet et al. 2014). Scenarios include four populations: Africa (Aaf), America (Aaa), Asia (Aaa), and Rabai (Aaa). N=32 for each sampled population. All samples available from Aaa Rabai were included. Subsampling was required from the larger populations (see Materials and Methods). T0 represents the most recent time point and increasing values of T go back in time. Scenario 1: Africa to America to Asia to Rabai; Scenario 2: Africa to Rabai (before Asia colonization); Scenario 3: Africa to America to Rabai (after Asia colonization); Scenario 4: Africa to America to Rabai (before Asia colonization); Scenario 5: Africa to Rabai (before America colonization); and Scenario 6: Africa to Rabai (after Asia colonization). Posterior probabilities are shown for each scenario. The best-fit scenario was Scenario 3. For more details see Materials and Methods and Table S5.

Figure S3: Discriminant Analysis of Principal Components showing two main genetic clusters: 1) the putative *Ae. aegypti queenlandensis* strain and 2) the main *Ae. aegypti* cluster including all Aaa and Aaf populations.